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Sequence Listing was accepted.
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Reviewer: Anne Corrigan
Timestamp: [year=2008; month=7; day=29; hr=14; min=47; sec=35; ms=461; ]
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Application No: 10527257   Version No: 5.0

Input Set:

Output Set:

Started: 2008-07-28 10:04:50.641

Finished: 2008-07-28 10:04:51.133

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 492 ms

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No. of SeqIDs Defined: 12

Actual SeqID Count: 12

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Leu Leu Leu Ser Ser Trp Cys Arg Thr Gly Leu Ala Asp Pro His Ser
            20   25   30

ctt tgc tat gac atc acc gtc atc cct aag ttc aga cct gga cca cgg   144
Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro Gly Pro Arg
        35   40   45

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Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr Phe Leu His Tyr
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gac tgt ggc agc aag aca gtc aca ccc gtc agt ccc ctg ggg aag aaa   240
Asp Cys Gly Ser Lys Thr Val Thr Pro Val Ser Pro Leu Gly Lys Lys
65   70   75   80

cta aat gtc aca acg gcc tgg aaa gca cag aac cca gta ctg aga gag   288
Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro Val Leu Arg Glu
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gtg gtg gac ata ctt aca gag caa ctg ctt gac att cag ctg gag aat   336
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cag aaa gcc gaa gga cac ggc agt gga tct tgg cag ctc agt ttc gat        432
Gln Lys Ala Glu Gly His Gly Ser Gly Ser Trp Gln Leu Ser Phe Asp
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gga cag atc ttc ctc ctc ttt gac tca gaa aac aga atg tgg aca acg        480
Gly Gln Ile Phe Leu Leu Phe Asp Ser Glu Asn Arg Met Trp Thr Thr
145                 150                 155                 160

gtt cat cct gga gcc aga aag atg aaa gaa aag tgg gag aat gac aag        528
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gat atg acc atg tcc ttc cat tac atc tca atg gga gac tgc aca gga        576
Asp Met Thr Met Ser Phe His Tyr Ile Ser Met Gly Asp Cys Thr Gly
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tgg ctt gag gac ttc ttg atg ggc atg gac agc acc ctg gag cca agt        624
Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser
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Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro Gly Pro Arg
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Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr Phe Leu His Tyr
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Asp Cys Gly Ser Lys Thr Val Thr Pro Val Ser Pro Leu Gly Lys Lys
65                  70                  75                  80
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Tyr Ile Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg Met Ser Cys Glu
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Gln Lys Ala Glu Gly His Gly Ser Gly Ser Trp Gln Leu Ser Phe Asp
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Gly Gln Ile Phe Leu Leu Phe Asp Ser Glu Asn Arg Met Trp Thr Thr
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Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys
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Asp Met Thr Met Ser Phe His Tyr Ile Ser Met Gly Asp Cys Thr Gly
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ctaaatgtca caacggcctg gaaagcacag aacccagtac tgagagaggt ggtggacata   300

cttacagagc aactgcttga cattcagctg gagaattaca tacccaagga acccctcacc   360

ctgcaggcca ggatgtcttg tgagcagaaa gccgaaggac acggcagtgg atcttggcag   420

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tccttccatt acatctcaat gggagactgc acaggatggc ttgaggactt cttgatgggc   600

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Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro Gly Pro Arg
        35   40   45

Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr Phe Leu His Tyr
    50   55   60

Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser Pro Leu Gly Lys Lys
65   70   75   80

Leu Asn Val Thr Thr Ala Trp Lys Ala Gln Asn Pro Val Leu Arg Glu

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                85                      90                      95


Val Val Asp Ile Leu Thr Glu Gln Leu Arg Asp Ile Gln Leu Glu Asn
            100                 105                 110


Tyr Thr Pro Lys Glu Pro Leu Thr Leu Gln Ala Arg Met Ser Cys Glu
            115                 120                 125


Gln Lys Ala Glu Gly His Ser Ser Gly Ser Trp Gln Phe Ser Phe Asp
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Gly Gln Ile Phe Leu Leu Phe Asp Ser Glu Lys Arg Met Trp Thr Thr
145                 150                 155                 160


Val His Pro Gly Ala Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys
                165                 170                 175


Val Val Ala Met Ser Phe His Tyr Phe Ser Met Gly Asp Cys Ile Gly
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Trp Leu Glu Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser
            195                 200                 205


Ala Gly Ala Pro Leu Ala Met Ser Ser Gly Thr Thr Gln Leu Arg Ala
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gttcatcctg gagccagaaa gatgaaagaa aagtgggaga atgacaaggt tgtggccatg      540

tccttccatt acttctcaat gggagactgt ataggatggc ttgaggactt cttgatgggc      600

atggacagca ccctggagcc aagtgcagga gcaccactcg ccatgtcctc aggcacaacc      660

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cctaagttca gacctggacc acggtggtgt gcggttcaag gccaggtgga tgaaaagact      180

tttcttcact atgactgtgg cagcaagaca gtcacacccg tcagtcccct ggggaagaaa      240

ctaaatgtca caacggcctg gaaagcacag aacccagtac tgagagaggt ggtggacata      300

cttacagagc aactgcttga cattcagctg gagaattaca tacccaagga acccctcacc      360

ctgcaggcca ggatgtcttg tgagcagaaa gccgaaggac acggcagtgg atcttggcag      420

ctcagtttcg atggacagat cttcctcctc tttgactcag aaaacagaat gtggacaacg      480

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